

Please amend claim 37 as follows:

37. (Amended) A method for detecting or quantifying a target nucleic acid in a sample by detecting signal from a plurality of labeled nucleotides incorporated into a primer comprising:

(a) selecting a nucleic acid having a target nucleotide base at a predetermined position in a template of a nucleic acid of interest;

(b) preparing an unlabeled primer complementary to a sequence immediately upstream of the target nucleotide base;

(c) treating a sample containing the nucleic acid of interest, if the nucleic acid is double-stranded, so as to obtain unpaired nucleotide bases spanning the specific position, or directly employing step (d) if the nucleic acid of interest is single-stranded;

(d) annealing the primer from (b) with the target nucleic acid from (c) under high stringency conditions to obtain a primer-nucleic acid duplex, wherein the target nucleotide base in the nucleic acid of interest is the first unpaired base immediately downstream of the 3' end of the primer;

(e) mixing the primer-nucleic acid duplex from (d) with a primer extension reaction reagent comprising: (i) three types of non-terminator nucleotides that are not complementarily matched to the target nucleotide, wherein at least one type of the non-terminator nucleotide is labeled with a detectable marker; and optionally (ii) one type of terminator nucleotide that is complementarily matched to the target nucleotide, wherein the terminator nucleotide is not labeled;

(f) performing the primer extension reaction by enzymatic or chemical means, wherein the incorporation of said non-terminator nucleotide and optionally, the terminator

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